

FIG. 1A

FIG. 1A

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ctcgctcctctcctacttggataactgtggtaattctagagctaatacatgccgacgggc 60
gctgaccccccttcgcggggggggatgcgtgcatttatcagatcaagaccaacccggtcagc 120
ccctctccggccccggccggggggcgggcgccggcggttttggtgactctagataacctc 180
gggccgatcgcacgccccccgtggcgggcgacgacccattcgaacgtctgccctatcaact 240
ttcgatggtagtcgccgtgcctaccatggtgaccacgggtgacggggaatcaggggttcga 300
ttccggagaggggagcctgagaaaacggctaccacatccaaggaaggcagcaggcgcgcaaa 360
ttacccactcccggaggtggcgggcgcccatcttggcgaaggggggatcaggaagtgcg 420
gaccgcggcgggcgggcgggcgggcgggcgggcgggcgagcccgagcgcaggccggaggctc 480
ccggcccgcggccccggagcggagcggagcggaggatgcagcagccgcagccgcagggg 540
cagcagcagccggggccggggcagcagctggggggccagggggcgggcgccggggggccggg 600
ggcgggccagggggggggcccgggggccggggccctgcctgaggcgagagctgaagctgctc 660
gagtccatcttccaccgcggccacgagcgcttccgcattgccagcgctgcctggacgag 720
ctgagctgcgagttcctgctggctggggccggagggggccggggcgggggccgcgcccga 780
ccgcatctccccccacgggggtcggtgcctggggatcctgtccgcatccactgcaacatc 840
acggagtcataccctgctgtgccccccatctggtcggtggagtctgatgaccctaacttg 900
gctgctgtcttgagagggctggtggacataaagaaaggaataactctgctattgcagcat 960
ctgaagaggatcatctccgacctgtgtaaactctataacctccctcagcatccagatgtg 1020
gagatgctggatcaacccttgccagcagagcagtgcacacaggaagacgtgtcttcagaa 1080
gatgaagatgaggagatgcctgaggacacagaagacttagatcactatgaaatgaaagag 1140
gaagagccagctgagggcaagaaatctgaagatgatggcattggaaaagaaaacttggcc 1200
atcctagagaaaaattaaaaagaaccagaggcaagattacttaaattggtgcagtgtctggc 1260
tcggtgcaggccactgaccggctgatgaaggagctcagggatataaccgatcacagagt 1320
ttcaaaggcggaactatgcagtcgaactcgtgaatgacagctctgtatgattggaatgtc 1380
aaactcctcaaagttgaccaggacagcgctttgcacaacgatctccagatcctcaaagag 1440

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FIG. 1B

aaagaaggagccgacttcattctacttaacttttcccttaagataactttccctttgac 1500
ccaccatttgtcagggttgtgtctccagtcctctctggaggggtatgttctgggcggaggg 1560
gccatctgcatggaacttctcaccaaacagggctggagcagtgccactccatagagtca 1620
gtgatcatgcagatcagtgccacactggtgaaggggaaagcacgagtgagtttggagcc 1680
aacaatctcaatacagtcctgacaagagcacagcagtcctacaagtccttggcagatc 1740
cacgaaaaaacggctggtacacacccccaaaagaagacggctaaccctggagtatcacc 1800
cttcctccctccccaggcaccactggaccaattacctttgaatgctgtatttggatctca 1860
cgctgcctctgtggttccctccctcatttttccctggacgtgatagctctgcctattgcag 1920
gacaatgatggctattctaaacgctaaggaaaaaaaacaaacacagaactgtttcaagta 1980
ctcaagactgacttacagaccaaccaaccaccttgctggaacccttgctagcaggcattc 2040
ttataaaagaaactttcgagcctccttatattgctggaaactcagctgtgctccagacta 2100
gagcctccttacctatgctatggatttttaatttattttctcttatttcatgtacactgc 2160
tttttttggttacagtgtatgatggatgtgtatgaaaaaatgtatctttgggaaaacaa 2220
ttacagtttgtaatttgaaaaaaaaaaaaaaaaa 2280

(SEQ ID NO:1)

FIG. 2A

CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
GCTGACCCCCCTTCGCGGGGGGGATGCGTGCATTTATCAGATCAAGACCAACCCGGTCAGC
CCCTCTCCGGCCCCCGCGGGGGGGCGGGCGCCGGCGGCTTTGGTGACTCTAGATAACCTC
GGGCCGATCGCACGCCCCCGTGGCGGCGACGACCCATTTCGAACGTCTGCCCTATCAACT
TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTTCA
TTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAA
TTACCCACTCCCGGAGGTGGCGGCGGCCATCTTGGCGAAGGGGGGATCAGGAAGTGCG
GACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGCCCGAGCGCAGGCCGAGGCTC
CCGGCCCCCGGCCCGGAGCGGAGCGGAGCGAGGATGCAGCAGCCGAGCCGAGGGG
M Q Q P Q P Q G
CAGCAGCAGCCGGGGCCGGGGCAGCAGCTGGGGGGCCAGGGGGCGGCGCCGGGGGCCGGG
Q Q Q P G P G Q Q L G G Q G A A P G A G
GGCGGCCAGGGGGGGGGCCCGGGGCCGGGGCCCTGCCTGAGGCGAGAGCTGAAGCTGCTC
G G P G G G P G P G P C L R R E L K L L
GAGTCCATCTTCCACCGCGGCCACGAGCGCTTCCGCATTGCCAGCGCTGCCTGGACGAG
E S I F H R G H E R F R I A S A C L D E
CTGAGCTGCGAGTTCTGCTGGCTGGGGCCGAGGGGCCGGGGCGGGGGCCGCGCCCGGA
L S C E F L L A G A G G A G A G A G A A P G
CCGCATCTCCCCCACGGGGGTCCGTGCCTGGGGATCCTGTCCGCATCCACTGCAACATC
P H L P P R G S V P G D P V R I H C N I
ACGAGTCATACCCTGCTGTGCCCCCATCTGGTCGGTGGAGTCTGATGACCCTAACTTG
T E S Y P A V P P I W S V E S D D P N L
GCTGCTGTCTTGGAGAGGCTGGTGGACATAAAGAAAGGGAATACTCTGCTATTGCAGCAT
A A V L E R L V D I K K G N T L L L Q H
CTGAAGAGGATCATCTCCGACCTGTGTAAACTCTATAACCTCCCTCAGCATCCAGATGTG
L K R I I S D L C K L Y N L P Q H P D V
GAGATGCTGGATCAACCCTTGCCAGCAGAGCAGTGCACACAGGAAGACGTGTCTTCAGAA
E M L D Q P L P A E Q C T Q E D V S S E
GATGAAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAAAGAG
D E D E E M P E D T E D L D H Y E M K E
GAAGAGCCAGCTGAGGGCAAGAAATCTGAAGATGATGGCATTGGAAAAGAAAACCTTGCC
E E P A E G K K S E D D G I G K E N L A
ATCCTAGAGAAAATTAAGAAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTCTGGC
I L E K I K K N Q R Q D Y L N G A V S G
TCGGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGT
S V Q A T D R L M K E L R D I Y R S Q S
TTCAAAGGCGGAAACTATGCAGTCAAACTCGTGAATGACAGTCTGTATGATTGGAATGTC
F K G G N Y A V E L V N D S L Y D W N V
AAACTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGAG
K L L K V D Q D S A L H N D L Q I L K E
AAAGAAGGAGCCGACTTCATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGAC
K E G A D F I L L N F S F K D N F P F D
CCACCATTTGTGAGGGTTGTCTCCAGTCTCTGAGGGGTATGTTCTGGGCGGAGGG
P P F V R V V S P V L S G G Y V L G G
GCCATCTGCAGTGAACCTTCTACCAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTCA
A I C M E L L T K Q G W S S A Y S I E S
GTGATCATGCAGATCAGTGCCCACTGGTGAAGGGGAAAGCACGAGTGCAGTTTGGAGCC
V I M Q I S A T L V K G K A R V Q F G A

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FIG. 2B

AACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTTGGTGCAGATC
N K S Q Y S L T R A Q Q S Y K S L V Q I
CACGAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGCTAACCCCTGGAGTATCACC
H E K N G W Y T P P K E D G *
CTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCA
CGCTGCCTCTGTGGTTCCCTCCCTCATTTCCTGGACGTGATAGCTCTGCCTATTGCAG
GACAATGATGGCTATTCTAAACGCTAAGGAAAAAAAACAAACACAGAACTGTTTCAAGTA
CTCAAGACTGACTTACAGACCAACCAACCACCTTGCTGGAACCCCTTGCTAGCAGGCATTC
TTATAAAAGAAACTTTTCGAGCCTCCTTATATTGCTGGAACTCAGCTGTGCTCCAGACTA
GAGCCTCCTTACCTATGCTATGGATTTTAAATTTATTTCTCTTATTTTCATGTACACTGC
TTTTTTTGGTTACAGTGTATGATGGATGTGTATGAAAAAATGTATCTTTGGGAAAAACAA
TTACAGTTTGTTAATTTGAAAAAAAAAAAAAAAAA

FIG. 3

MQQPQPQGQQ	QPGPGQQLGG	QGAAPGAGGG	PGGGPGPGPC	40
LRRELKLLES	IFHRGHERFR	IASACLDELS	CEFLAGAGG	80
AGAGAAPGPH	LPPRGSVPGD	PVRIHCNITE	SYPAVPPIWS	120
VESDDPNLAA	VLERLVDIKK	GNTLLLQHLK	RIISDLCKLY	160
NLPQHDPVEM	LDQPLPAEQC	TQEDVSSEDE	DEEMPEDTED	200
LDHYEMKEEE	PAEGKKSEDD	GIGKENLAIL	EKIKKNQRQD	240
YLNGAVSGSV	QATDRLMKEL	RDIYRSQSFK	GGNYAVELVN	280
DSLYDWNVKL	LKVDQDSALH	NDLQILKEKE	GADFILLNFS	320
FKDNFPFDPP	FVRVSPVLS	GGYVLGGGAI	CMELLTKQGW	360
SSAYSIESVI	MQISATLVKG	KARVQFGANK	SQYSLTRAQQ	400
SYKSLVQIHE	KNGWYTPPKE	DG		422

(SEQ ID NO:2)

FIG. 3

FIG. 4

T0620T "6455000T"

RATL1d6	(1)	1	MOQPQPOGQQQPGPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLLESIFHRGHERFRITASAC	65
T21349_F25H2.8_Cel	(1)		-----MACLRKLKEDIQVLEKLFPKNHNRFOILLSAS	
AAF45767_EG:25E8_Dr	(1)		-----MACLNTLKQEIKTLEKIFPKNHFRFOILNSS	
RATL1d6	(66)	66	LDELSCFLLLAGAGGAGAGAAPGPHLPGRGVPVGDVRIHCNITESYPAPVPPVWSVESDDPNLAA	130
T21349_F25H2.8_Cel	(32)		VDEL SMKFINAEN-----KG-----IIVTANTIQENYPRQPPVWFSESDDVVIG	
AAF45767_EG:25E8_Dr	(32)		VDELLCRFIDKNG-----KR-----YDIHANITETYPSSPPVWFAESEETSVTN	
RATL1d6	(131)	131	VLERLVDIKKGNTLLQLHLKRIISDLCKLYNLPHQHPDVEMLDQPL-----	195
T21349_F25H2.8_Cel	(76)		MSLQRLTETEESTNHLHVRLVSDLCSEFYNLQMPCELPQIAPPVRDD-----IDEGRGSDI	
AAF45767_EG:25E8_Dr	(76)		AVQILSNTNGRDNHVINQVGILLRELRLHNVPPLPDIDNLALPLQTPPPSASPLRCEQRPGGGG	
RATL1d6	(176)	196	-----PAEQCTQEDVSSSEDEEEMPEDTEDLDHYEMKEEPEAEGKKSEDDGIGKENLAILEKIK	260
T21349_F25H2.8_Cel	(133)		SDTTSEPIDDDMAGDGEVDDDEEEEDDEDADGDIEIVEMAEEDPTSQHDVGVSKEGLDMLDKVS	
AAF45767_EG:25E8_Dr	(141)		AGGGGGPHGNEETSDSQEEIEDPIGESEGESEGEDLPLEMDDVRSTSKKDDMEVEHLATLEKLR	
P52483_UB6B_MOUSE	(1)		-----MSSDRQRSDDSPSTSSGSSDADQRDP	
RATL1d6	(235)	261	KNQRQDYLNCAVSGSVQATDRMLKELRDIYRSQSFKGGNYAVELVN-DSLVDNVLKLVQDQSA	325
T21349_F25H2.8_Cel	(198)		KINRQOHLDGKVGSGSITATDRMLKEIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDS	
AAF45767_EG:25E8_Dr	(206)		QSQRQDYLNKGSVSGSVQATDRMLKELRDIYRSDAFKKNMYSIELVN-ESIYEWNIKLKSVDPD	
P52483_UB6B_MOUSE	(28)		AAPKPEEQEERKPSATQCKKNTKLSSKTTAKLSTSAKRICKELAEITLDPPPNCSSAGEKCDNIYE	
P27924_UBC1_HUMAN	(1)		-----MANIAVQRIKREFKEVLKSEETSKNQIKVDLVD-----ENFT-E	
CAA72184_UBCD4_Dr	(1)		-----MANMAVSRIRKREFKEVMRSEEIVQCSIKIELVN-----DSWTE	
P14682_UBC3_YEAST	(1)		-----MSSRKSTASSLLRLQYRELTDPKKAI PSFHIELEDD-----SNIFTW	
RATL1d6	(299)	326	LHNDLQILKEKEGA-DFILLNFSFKDNFPFPPFVRVVSFVLSGGYVLGGGAICMELLTKQG---	390
T21349_F25H2.8_Cel	(263)		LFEDMKRLKKDHNQ-DHLLFSFTFNEKFPDPPFVRVVAAPHINQGFVLGGGAICMELLTKQG---	
AAF45767_EG:25E8_Dr	(270)		LHSDLOMLKEKEGK-DSILLNLFKEKTYPFEPFVRVWHPIISGGYVLGGGAICMELLTKQG---	
P52483_UB6B_MOUSE	(93)		WRSTILGPPGVSVEGCVFFLDTHSSDYPFKPPKVTFRTRTYHCNINSQ-GVICLDILKDN----	
P27924_UBC1_HUMAN	(39)		LRGETAGPPDTPYEGGRYQLEIKIPETYPFNPVKVRFITRIWHPNISSVTGAICLDILKDKQ----	
CAA72184_UBCD4_Dr	(39)		LRGETAGPPDTPYEGGKFVLEIKVPETYPFNPVKVRFITRIWHPNISSVTGAICLDILKDN----	
P14682_UBC3_YEAST	(43)		NIGVMVLNEDSIYHGGFFKAQMRFPEDFPFSPPOFRFTPATYHPNVYRD-CRLCISILHQSGDPM	
RATL1d6	(360)	391	-----WSSAYSTIESVIMQISATLVKKGKARVQFCANK-----SQYSLTRAQQSYKSLVQI	455
T21349_F25H2.8_Cel	(324)		-----WSSAYSTIESCILQIAATLVKGRARISFDAKHT-----STYSMARAAQQSEKSLQOI	
AAF45767_EG:25E8_Dr	(331)		-----WSSAYTVEAVIMQIAATLVKKGKARIQFGATKALTQ----GOYSLARAQQSFKSLVQI	
P52483_UB6B_MOUSE	(153)		-----WSPALTTSKVLLSICSLLTDCNPADFLVGSIA-----QYLTNRAEHDRIARQWT	
P27924_UBC1_HUMAN	(100)		-----WAAAMTLRTVLLSLQALLAAAEPPDQDAVVAN-----QYKONPEMFKQIARLWA	
CAA72184_UBCD4_Dr	(100)		-----WAAAMTLRTVLLSLQALLAAAEPPDQDAVVAY-----QFKDKYDLFLLTAKHWT	
P14682_UBC3_YEAST	(107)		TDEPDAETWSPVQTVESVLISIVSLLEDPNINSANVDAADVDRKNPEQYKQRVKMEVERSKQDI	
RATL1d6	(409)	456	HEKNGWYTPPKEDG-----	520
T21349_F25H2.8_Cel	(374)		HAKSGCTFLCSTPSSHFFALHLVFFLHSDDDFFNGFLKSETFTFFKL SFRGYISSLVLYSFSRHL	
AAF45767_EG:25E8_Dr	(384)		HEKNGWYTPPKEDG-----	
P52483_UB6B_MOUSE	(203)		KRYAT-----	
P27924_UBC1_HUMAN	(150)		HVYAGAPVSSPEYTKKIENLCAMGFDRNAVIVALSSKSWDVE TATELLLSN-----	
CAA72184_UBCD4_Dr	(150)		NAYACGPHTFPDCDSKIQRDRMDGIDEHEARAVLSKENWNLEKATEGLFS-----	
P14682_UBC3_YEAST	(172)		PKGFIPTSESAYISQSKLDEPESNKDMADNFWYDSLDLDDDENGSVILQDDDYDDGNNHIPFEDD	
T21349_F25H2.8_Cel	(439)	521	HHPFFTRFLIPQLQPPPIPFQLIPPFLNRTKHV-----	579
P14682_UBC3_YEAST	(237)		DVYNYNDNDDDDERIEFEDDDDDDDSIDNDSVMDRKQPHKADESEDEVVERVSKKI	

FIG. 5A

RATL1d6 BLAST results/alignment w/ Drosophila protein

>GCGPROT:O46068 EG:25E8.2 PROTEIN.

Length = 394

Score = 369 bits (936), Expect = e-101

Identities = 194/403 (48%), Positives = 265/403 (65%), Gaps = 51/403 (12%)

Query: 41 LRRELKLLSIFHRGHERFRIASACDELSCFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100
L++E+K LE IF + HERF+I ++ +DEL C F+ G
Sbjct: 7 LKQEIKTLEKIFPKNHERFQILNSSVDELLCRFI-----DKNKG 45

Query: 101 PVRIHCNITESYPVPPPIWSVESDDPNLAAVLERLVDIKKGNLTLLQLHLKRIISDLCKLY 160
IH NITE+YP+ PP+W ES++ ++ ++ L + + ++ + ++ +LC+L+
Sbjct: 46 RYDIHANITETYPSSPPVWFAESEETSVTNAVQILSNTNGRDNHVINQVGILLRELCLRH 105

Query: 161 NLPQHDPDVEMLDQPLPAEQCTQEDVSSDE-----DEMPEDTEDLDHYEM 206
N+P PD++ L PL + + E +EE D E+++
Sbjct: 106 NVPLPPDIDNLALPLQTPPPSASPLRCEQRPGGGGAGGGGGPHGNEETDSDQEEIEDPIG 165

Query: 207 KEEEPAGGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNQAVSGSVQATD 254
+ E+ +EG + S+ D + E+LA LEK++++QRQDYL G+VSGSVQATD
Sbjct: 166 ESEQESEGDEDLPLEMDDVRSTSKKDDMEVEHLATLEKLRQSRQDYLKGSVSGSVQATD 225

Query: 255 RLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKKLKVQDSALHNDLQILKEKEGADF 314
RLMKELRDIYRS +FK Y++ELVN+S+Y+WN++L VD DS LH+DLQ+LKEKEG D
Sbjct: 226 RLMKELRDIYRSDAFKKNMYSIELVNESIYEWNI RLKSVDPDSPLHSDLQMLKEKEGKDS 285

Query: 315 ILLNFSFKDNFPFDPFVRVVSPLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS 374
ILLN FK+ +PF+PPFVRVV P++SGGYVL GGAICMELLTKQGWSSAY++E+VIMQI+
Sbjct: 286 ILLNILFKETYPFEPFVRVWHPIISGGYVLIGGAICMELLTKQGWSSAYTVEAVIMQIA 345

Query: 375 ATLVKGKARVQFGANKS----QYSLTRAQQSYKSLVQIHEKNG 413
ATLVKGKAR+QFGA K+ QYSL RAQQS+KSLVQIHEKNG
Sbjct: 346 ATLVKGKARIQFGATKALTQGQYSLARAQQSFKSLVQIHEKNG 388

FIG. 5B

RATL1d6 BLAST results/alignment w/ C. elegans protein

>GCGPROT:Q93571 F25H2.8 PROTEIN.

Length = 471

Score = 317 bits (805), Expect = 6e-86

Identities = 178/397 (44%), Positives = 247/397 (61%), Gaps = 49/397 (12%)

Query: 41 LRRELKLLSIFHRGHERFRIASACLDLSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100
L+ ++++LE +F + H RF+I SA +DELS +F+ A G
Sbjct: 7 LKEDIQVLEKLFPKNHNRFQILSASVDELSMKFINAENKG----- 46

Query: 101 PVRIHCNITESYPAPVPIWSVESDD-PNLA AVLRLVDIKKNTLLLQHLKRIISDLCKL 159
+ + NI E+YP PPIW ESDD P + L+RL + ++ +T +L + R++SDLC
Sbjct: 47 -IIVTANIQENYPRQPPIWFSESDDVPIGMSLQRLTETEE-STNILHQVHRLVSDLCSEF 104

Query: 160 YNL-----PQHPDVE-----MLDQPLPAEQCTQEDVSSSEDEDEEMPEDTE 199
YNL P D++ +P+ + +V +DE+EE ED +
Sbjct: 105 YNLQMPCELPQIAPPVRDDIDEGRGSDISDTTSEPIDDDMAGDGEVDDDDDEEEDDEDAD 164

Query: 200 -DLDHYEMKEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNQAVSGSVQATDRLMK 258
D++ EM EE+P D G+ KE L +L+K+ K RQ +L+G V GS+ ATDRLMK
Sbjct: 165 GDIEIVEMAEEDPTS---QHDVGVSKEGLDMLDKVSKINRQQHLDGKVQGSITATDRLMK 221

Query: 259 ELRDIYRSQSFKGGNYAVELVND-SLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILL 317
E+RDI+RS+ FK G Y EL + +LY W +KL KVD+DS L D++ LK+ D +L
Sbjct: 222 EIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDSPLFEDMKKLKDHNDHLLF 281

Query: 318 NFSFKDNFPDPPFVRVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATL 377
+F+F + FP DPPFVRVV+P ++ G+VLGGGAICMELLTKQGWSSAYSIES I+QI+ATL
Sbjct: 282 SFTTFNEKFPDPPFVRV VAPHINQGFVLGGGAICMELLTKQGWSSAYSIESCILQIAATL 341

Query: 378 VKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413
VKG+AR+ F A + S YS+ RAQQS+KSL QIH K+G
Sbjct: 342 VKGRARISFDAKHTSTYSMARAAQSFKSLQQIHAKSG 378

FIG. 5B

FIG. 6

Relative Expression of RATL1d6

